OIPE

RAW SEQUENCE LISTING   DATE: 09/23/2002
PATENT APPLICATION: US/09/823,394   TIME: 10:20:32

          Input Set : A:\SALKINS.012CP1.TXT
          Output Set: N:\CRF3\09232002\I823394.raw

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  4 <110> APPLICANT: Chory, Joanne
  5        Jianming, Li
  6        Salk Institute for Biological Studies
  8 <120> TITLE OF INVENTION: RECEPTOR KINASE, BIN 1
 11 <130> FILE REFERENCE: SALKINS.012CP1
 13 <140> CURRENT APPLICATION NUMBER: US/09/823,394       C-->
 13 <141> CURRENT FILING DATE: 2001-03-30                 C-->
 13 <150> PRIOR APPLICATION NUMBER: 08/881,706
 14 <151> PRIOR FILING DATE: 1997-06-24
 16 <160> NUMBER OF SEQ ID NOS: 2
 18 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 4104
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Arabidopsis
 25 <220> FEATURE:
 26 <221> NAME/KEY: CDS
 27 <222> LOCATION: (97)...(3684)
 29 <400> SEQUENCE: 1
 30 cttccacttc ctctgtaatg gtggaaccaa aaccctagat tcccccttc atcttctcta 60
 31 cttcccacac ttttctctct cacaaactct tgagaa atg aag act ttt tca agc 114
 32                                          Met Lys Thr Phe Ser Ser
 33                                           1               5
 35 ttc ttt ctc tct gta aca act ctc ttc ttc ttc tcc ttc ttt tct ctt 162
 36 Phe Phe Leu Ser Val Thr Thr Leu Phe Phe Phe Ser Phe Phe Ser Leu
 37              10              15              20
 39 tca ttt caa gct tca cca tct cag tct tta tac aga gaa atc cat cag 210
 40 Ser Phe Gln Ala Ser Pro Ser Gln Ser Leu Tyr Arg Glu Ile His Gln
 41          25              30              35
 43 ctt ata agc ttc aaa gac gtt ctt cct gac aag aat ctt ctc cca gac 258
 44 Leu Ile Ser Phe Lys Asp Val Leu Pro Asp Lys Asn Leu Leu Pro Asp
 45      40              45              50
 47 tgg tct tcc aac aaa aac ccg tgt act ttc gat ggc gtt act tgc aga 306
 48 Trp Ser Ser Asn Lys Asn Pro Cys Thr Phe Asp Gly Val Thr Cys Arg
 49 55              60              65              70
 51 gac gac aaa gtt act tcg att gat ctc agc tcc aag cct ctc aac gtc 354
 52 Asp Asp Lys Val Thr Ser Ile Asp Leu Ser Ser Lys Pro Leu Asn Val
 53              75              80              85
 55 gga ttc agt gcc gtg tcc tcg tct ctc ctg tct ctc acc gga tta gag 402
 56 Gly Phe Ser Ala Val Ser Ser Ser Leu Leu Ser Leu Thr Gly Leu Glu
 57              90              95              100
 59 tct ctg ttt ctc tca aac tca cac atc aat ggc tcc gtt tct ggc ttc 450
 60 Ser Leu Phe Leu Ser Asn Ser His Ile Asn Gly Ser Val Ser Gly Phe
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61          105                   110                  115
63 aag tgc tct gct tct tta acc agc ttg gat cta tct aga aac tct ctt    498
64 Lys Cys Ser Ala Ser Leu Thr Ser Leu Asp Leu Ser Arg Asn Ser Leu
65      120                   125                  130
67 tcg ggt cct gta acg act cta aca agc ctt ggt tct tgc tcc ggt ctg    546
68 Ser Gly Pro Val Thr Thr Leu Thr Ser Leu Gly Ser Cys Ser Gly Leu
69 135                   140                   145                  150
71 aag ttt ctt aac gtc tct tcc aat aca ctt gat ttt ccc ggg aaa gtt    594
72 Lys Phe Leu Asn Val Ser Ser Asn Thr Leu Asp Phe Pro Gly Lys Val
73                   155                   160                  165
75 tca ggt ggg ttg aag cta aac agc ttg gaa gtt ctg gat ctt tct gcg    642
76 Ser Gly Gly Leu Lys Leu Asn Ser Leu Glu Val Leu Asp Leu Ser Ala
77              170                   175                  180
79 aat tca atc tcc ggt gct aac gtc gtt ggt tgg gtt ctc tcc gat ggg    690
80 Asn Ser Ile Ser Gly Ala Asn Val Val Gly Trp Val Leu Ser Asp Gly
81          185                   190                  195
83 tgt gga gag ttg aaa cat tta gcg att agc gga aac aaa atc agt gga    738
84 Cys Gly Glu Leu Lys His Leu Ala Ile Ser Gly Asn Lys Ile Ser Gly
85      200                   205                  210
87 gac gtc gat gtt tct cgc tgc gtg aat ctc gag ttt ctc gat gtt tcc    786
88 Asp Val Asp Val Ser Arg Cys Val Asn Leu Glu Phe Leu Asp Val Ser
89 215                   220                   225                  230
91 tcc aac aat ttc tcc act ggg att cct ttc ctc gga gat tgc tct gct    834
92 Ser Asn Asn Phe Ser Thr Gly Ile Pro Phe Leu Gly Asp Cys Ser Ala
93                   235                   240                  245
95 ctg caa cat ctt gac atc tcc ggg aac aaa tta tcc ggc gat ttc tcc    882
96 Leu Gln His Leu Asp Ile Ser Gly Asn Lys Leu Ser Gly Asp Phe Ser
97              250                   255                  260
99 cgt gct atc tct act tgc aca gag ctc aag ttg ttg aac atc tct agt    930
100 Arg Ala Ile Ser Thr Cys Thr Glu Leu Lys Leu Leu Asn Ile Ser Ser
101          265                   270                  275
103 aac caa ttc gtc gga cca atc cct ccg cta ccg ctt aaa agt ctc caa   978
104 Asn Gln Phe Val Gly Pro Ile Pro Pro Leu Pro Leu Lys Ser Leu Gln
105      280                   285                  290
107 tac ctc tct ctg gcc gag aac aaa ttc acc ggc gag atc cct gac ttt   1026
108 Tyr Leu Ser Leu Ala Glu Asn Lys Phe Thr Gly Glu Ile Pro Asp Phe
109 295                   300                   305                  310
111 ctc tcc ggc gcg tgt gat aca ctc act ggt ctc gat ctc tct gga aat   1074
112 Leu Ser Gly Ala Cys Asp Thr Leu Thr Gly Leu Asp Leu Ser Gly Asn
113                   315                   320                  325
115 cat ttc tac ggt gcg gtt cct cca ttc ttc ggt tca tgt tct ctt ctc   1122
116 His Phe Tyr Gly Ala Val Pro Pro Phe Phe Gly Ser Cys Ser Leu Leu
117              330                   335                  340
119 gaa tca ctc gcg ttg tcg agt aac aac ttc tct ggc gag tta ccg atg   1170
120 Glu Ser Leu Ala Leu Ser Ser Asn Asn Phe Ser Gly Glu Leu Pro Met
121          345                   350                  355
123 gat acg ttg ttg aag atg aga gga ctc aaa gta ctt gat ctg tct ttc   1218
124 Asp Thr Leu Leu Lys Met Arg Gly Leu Lys Val Leu Asp Leu Ser Phe
125      360                   365                  370
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127 aac gag ttt tcc ggc gaa tta ccg gaa tct ctg acg aat cta tcc gct   1266
128 Asn Glu Phe Ser Gly Glu Leu Pro Glu Ser Leu Thr Asn Leu Ser Ala
129 375             380             385             390
131 tcg ttg cta acg tta gat ctc agc tcc aac aat ttc tcc ggt ccg att   1314
132 Ser Leu Leu Thr Leu Asp Leu Ser Ser Asn Asn Phe Ser Gly Pro Ile
133             395             400             405
135 ctc cca aat ctc tgc cag aac cct aaa aac act ctg cag gag ctt tac   1362
136 Leu Pro Asn Leu Cys Gln Asn Pro Lys Asn Thr Leu Gln Glu Leu Tyr
137             410             415             420
139 ctt cag aac aat ggc ttc acc ggg aag att cca ccg act tta agc aac   1410
140 Leu Gln Asn Asn Gly Phe Thr Gly Lys Ile Pro Pro Thr Leu Ser Asn
141         425             430             435
143 tgt tct gag ctg gtt tcg ctt cac ttg agc ttc aat tac ctc tcc ggg   1458
144 Cys Ser Glu Leu Val Ser Leu His Leu Ser Phe Asn Tyr Leu Ser Gly
145     440             445             450
147 aca atc cct tcg agc tta ggc tct cta tcg aag ctt cga gat ctg aaa   1506
148 Thr Ile Pro Ser Ser Leu Gly Ser Leu Ser Lys Leu Arg Asp Leu Lys
149 455             460             465             470
151 cta tgg ctg aat atg tta gaa gga gag atc cct cag gag ctc atg tat   1554
152 Leu Trp Leu Asn Met Leu Glu Gly Glu Ile Pro Gln Glu Leu Met Tyr
153             475             480             485
155 gtc aag acc tta gag act ctg atc ctc gac ttc aac gat tta acc ggt   1602
156 Val Lys Thr Leu Glu Thr Leu Ile Leu Asp Phe Asn Asp Leu Thr Gly
157         490             495             500
159 gaa atc cct tcc ggt tta agt aac tgt acc aat ctt aac tgg att tct   1650
160 Glu Ile Pro Ser Gly Leu Ser Asn Cys Thr Asn Leu Asn Trp Ile Ser
161         505             510             515
163 ctg tcg aat aac cgg tta acc ggt gag att ccg aaa tgg att ggc cgg   1698
164 Leu Ser Asn Asn Arg Leu Thr Gly Glu Ile Pro Lys Trp Ile Gly Arg
165     520             525             530
167 tta gag aat ctc gct atc ctc aag tta agc aac aat tca ttc tcc ggg   1746
168 Leu Glu Asn Leu Ala Ile Leu Lys Leu Ser Asn Asn Ser Phe Ser Gly
169 535             540             545             550
171 aac att ccg gat gag ctc ggc gac tgc aga agc tta atc tgg ctt gat   1794
172 Asn Ile Pro Asp Glu Leu Gly Asp Cys Arg Ser Leu Ile Trp Leu Asp
173             555             560             565
175 ctc aac acc aat ctc ttc aat gga acg att ccg gcg gcg atg ttt aaa   1842
176 Leu Asn Thr Asn Leu Phe Asn Gly Thr Ile Pro Ala Ala Met Phe Lys
177         570             575             580
179 caa tcc ggg aaa atc gct gcc aat ttc atc gcc ggt aag agg tac gtt   1890
180 Gln Ser Gly Lys Ile Ala Ala Asn Phe Ile Ala Gly Lys Arg Tyr Val
181         585             590             595
183 tat atc aaa aac gat ggg atg aag aaa gag tgt cat gga gct ggt aat   1938
184 Tyr Ile Lys Asn Asp Gly Met Lys Lys Glu Cys His Gly Ala Gly Asn
185     600             605             610
187 tta ctt gag ttt caa gga atc aga tcc gaa caa tta aac cgg ctt tca   1986
188 Leu Leu Glu Phe Gln Gly Ile Arg Ser Glu Gln Leu Asn Arg Leu Ser
189 615             620             625             630
191 acg agg aac cct tgt aat atc act agc aga gtc tat gga ggt cac act   2034
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192 Thr Arg Asn Pro Cys Asn Ile Thr Ser Arg Val Tyr Gly Gly His Thr
193             635             640             645
195 tcg ccg acg ttt gat aac aat ggt tcg atg atg ttt ctg gac atg tct      2082
196 Ser Pro Thr Phe Asp Asn Asn Gly Ser Met Met Phe Leu Asp Met Ser
197             650             655             660
199 tac aac atg ttg tct gga tac ata ccg aag gag att ggt tcg atg cct      2130
200 Tyr Asn Met Leu Ser Gly Tyr Ile Pro Lys Glu Ile Gly Ser Met Pro
201             665             670             675
203 tat ctg ttt att ctc aat ttg ggt cat aac gat atc tct ggt tcg att      2178
204 Tyr Leu Phe Ile Leu Asn Leu Gly His Asn Asp Ile Ser Gly Ser Ile
205         680             685             690
207 cct gat gag gta ggt gat cta aga ggt tta aac att ctt gat ctt tca      2226
208 Pro Asp Glu Val Gly Asp Leu Arg Gly Leu Asn Ile Leu Asp Leu Ser
209 695             700             705             710
211 agc aat aag ctc gat ggg agg att cct cag gct atg tca gct ctt act      2274
212 Ser Asn Lys Leu Asp Gly Arg Ile Pro Gln Ala Met Ser Ala Leu Thr
213             715             720             725
215 atg ctt acg gaa atc gat ttg tcg aat aat aat ttg tct ggt ccg att      2322
216 Met Leu Thr Glu Ile Asp Leu Ser Asn Asn Asn Leu Ser Gly Pro Ile
217             730             735             740
219 cct gag atg ggt cag ttt gag act ttt cca ccg gct aag ttc ttg aac      2370
220 Pro Glu Met Gly Gln Phe Glu Thr Phe Pro Pro Ala Lys Phe Leu Asn
221             745             750             755
223 aat cct ggt ctc tgt ggt tat cct ctt ccg cgg tgt gat cct tca aat      2418
224 Asn Pro Gly Leu Cys Gly Tyr Pro Leu Pro Arg Cys Asp Pro Ser Asn
225         760             765             770
227 gca gac ggt tat gct cat cat cag aga tct cat gga agg aga cca gcg      2466
228 Ala Asp Gly Tyr Ala His His Gln Arg Ser His Gly Arg Arg Pro Ala
229 775             780             785             790
231 tcc ctt gct ggt agt gtg gcg atg gga ttg ttg ttc tct ttt gtg tgt      2514
232 Ser Leu Ala Gly Ser Val Ala Met Gly Leu Leu Phe Ser Phe Val Cys
233             795             800             805
235 ata ttt ggg ctg atc ctt gtt ggt aga gag atg agg aag aga cgg aga      2562
236 Ile Phe Gly Leu Ile Leu Val Gly Arg Glu Met Arg Lys Arg Arg Arg
237             810             815             820
239 aag aaa gag gcg gag ttg gag atg tat gcg gaa gga cat gga aac tct      2610
240 Lys Lys Glu Ala Glu Leu Glu Met Tyr Ala Glu Gly His Gly Asn Ser
241             825             830             835
243 ggc gat aga act gct aac aac acc aat tgg aag ctg act ggt gtg aaa      2658
244 Gly Asp Arg Thr Ala Asn Asn Thr Asn Trp Lys Leu Thr Gly Val Lys
245         840             845             850
247 gaa gcc ttg agt atc aat ctt gct gct ttc gag aag cca ttg cgg aag      2706
248 Glu Ala Leu Ser Ile Asn Leu Ala Ala Phe Glu Lys Pro Leu Arg Lys
249 855             860             865             870
251 ctc acg ttt gcg gat ctt ctt cag gct acc aat ggt ttc cat aat gat      2754
252 Leu Thr Phe Ala Asp Leu Leu Gln Ala Thr Asn Gly Phe His Asn Asp
253             875             880             885
255 agt ctg att ggt tct ggt ggg ttt gga gat gtt tac aaa gcg att ttg      2802
256 Ser Leu Ile Gly Ser Gly Gly Phe Gly Asp Val Tyr Lys Ala Ile Leu
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257              890              895              900
259 aaa gat gga agc gcg gtg gct atc aag aaa ctg att cat gtt agc ggt   2850
260 Lys Asp Gly Ser Ala Val Ala Ile Lys Lys Leu Ile His Val Ser Gly
261         905              910              915
263 caa ggt gat aga gag ttc atg gcg gag atg gaa acc att ggg aag atc   2898
264 Gln Gly Asp Arg Glu Phe Met Ala Glu Met Glu Thr Ile Gly Lys Ile
265         920              925              930
267 aaa cat cga aat ctt gtg cct ctt ctt ggt tat tgc aaa gtt gga gac   2946
268 Lys His Arg Asn Leu Val Pro Leu Leu Gly Tyr Cys Lys Val Gly Asp
269 935              940              945              950
271 gag cgg ctt ctt gtt aat gag gtt atg aag tat gga agt tta gaa gat   2994
272 Glu Arg Leu Leu Val Asn Glu Val Met Lys Tyr Gly Ser Leu Glu Asp
273              955              960              965
275 gtt ttg caa gac ccc aag aaa ggt ggg gtg aaa ctt aaa ttg tcc aca   3042
276 Val Leu Gln Asp Pro Lys Lys Gly Gly Val Lys Leu Lys Leu Ser Thr
277              970              975              980
279 cgg cgg aag att gcg ata gga tca gct aga ggg ctt gct ttc ctt cac   3090
280 Arg Arg Lys Ile Ala Ile Gly Ser Ala Arg Gly Leu Ala Phe Leu His
281         985              990              995
283 cac aac tgc agt ccg cat atc atc cac aga gac atg aaa tcc agt aat   3138
284 His Asn Cys Ser Pro His Ile Ile His Arg Asp Met Lys Ser Ser Asn
285         1000             1005             1010
287 gtg ttg ctt gat gag aat ttg gaa gct cgg gtt tca gat ttt ggc atg   3186
288 Val Leu Leu Asp Glu Asn Leu Glu Ala Arg Val Ser Asp Phe Gly Met
289 1015             1020             1025             1030
291 gcg agg ctg atg agt gcg atg gat acg cat tta agc gtc agt aca tta   3234
292 Ala Arg Leu Met Ser Ala Met Asp Thr His Leu Ser Val Ser Thr Leu
293              1035             1040             1045
295 gct ggt aca ccg ggt tac gtt cct cca gag tat tac caa agt ttc agg   3282
296 Ala Gly Thr Pro Gly Tyr Val Pro Pro Glu Tyr Tyr Gln Ser Phe Arg
297              1050             1055             1060
299 tgt tca aca aaa gga gac gtt tat agt tac ggt gtg gtc tta ctc gag   3330
300 Cys Ser Thr Lys Gly Asp Val Tyr Ser Tyr Gly Val Val Leu Leu Glu
301         1065             1070             1075
303 cta ctc acg ggt aaa cgg cca acg gat tca ccg gat ttt gga gat aac   3378
304 Leu Leu Thr Gly Lys Arg Pro Thr Asp Ser Pro Asp Phe Gly Asp Asn
305         1080             1085             1090
307 aac ctt gtt gga tgg gtg aaa cag cac gca aaa ctg cgg att agc gat   3426
308 Asn Leu Val Gly Trp Val Lys Gln His Ala Lys Leu Arg Ile Ser Asp
309 1095             1100             1105             1110
311 gtg ttt gac ccg gag ctt atg aag gaa gat cca gca tta gag atc gaa   3474
312 Val Phe Asp Pro Glu Leu Met Lys Glu Asp Pro Ala Leu Glu Ile Glu
313              1115             1120             1125
315 ctt tta caa cat tta aaa gtt gcg gtt gcg tgt ttg gat gat cgg gct   3522
316 Leu Leu Gln His Leu Lys Val Ala Val Ala Cys Leu Asp Asp Arg Ala
317              1130             1135             1140
319 tgg aga cga ccg aca atg gta caa gtc atg gcc atg ttt aag gag ata   3570
320 Trp Arg Arg Pro Thr Met Val Gln Val Met Ala Met Phe Lys Glu Ile
321         1145             1150             1155
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L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date